**Amendments to the Claims**

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-11 (cancelled)

12. (Currently Amended) A method for generating a secondary library of protein variants of a target protein comprising:

a) inputting the three dimensional coordinates of said target protein into a computer;

b) utilizing a forcefield calculation to generate a primary library comprising a plurality of primary variant amino acid residues at primary variant positions; and

c) ~~computationally generating a probability distribution table of variant amino acid residues in a plurality of said primary variant positions; and~~

~~d)~~ combining a plurality of said primary variant amino acid residues from step b) to generate a secondary library of secondary variant proteins, wherein at least one of said secondary variant proteins is different from the primary variant proteins.

13. (Currently Amended) A method according to claim 12, wherein said force field calculation is a Self-Consistent Mean Field (SCMF) calculation.

Claims 14-20 (Cancelled)

21. (Currently Amended) A method according to claim 12, further comprising synthesizing a plurality of said secondary variant proteins, wherein said combining comprises:

~~a~~e) generating a set of oligonucleotide probes each encoding at least one of said primary variant amino acid residues;

~~b~~f) using said probes in a polymerase chain reaction (PCR) to generate a plurality of oligonucleotide sequences, each encoding said secondary variant sequences; and

~~c~~g) producing said secondary variant sequences in host cells transformed with said oligonucleotide sequences.

22. (Previously presented) A method according to claim 21 wherein said PCR is multiple PCR wherein said probes are pooled.

23. (Previously presented) A method according to 22 wherein said probes are added in equimolar amounts.

24. (Currently Amended) A method according to claim ~~23~~ 22 wherein said probes are combined in amounts that correspond to the frequency of the said variant amino acid residues in said ~~probability distribution table~~ secondary library.

Claims 25-32 (cancelled)

33. (New) A method for generating a secondary library of protein variants of a target protein comprising:
a) inputting the three dimensional coordinates of said target protein into a computer;
b) utilizing a forcefield calculation to generate a primary library comprising a plurality of primary variant amino acid residues at primary variant positions; and
c) combining a plurality of said primary variant amino acid residues from step b) to generate a secondary library of secondary variant proteins.

34. (New) A method for generating a secondary library of protein variants of a target protein comprising:
a) inputting the three dimensional coordinates of said target protein into a computer;
b) utilizing a forcefield calculation to generate a primary library comprising a plurality of primary variant amino acid residues at primary variant positions; and
c) computationally processing a plurality of said primary variant amino acid residues from step b) to generate a secondary library of secondary variant proteins.

35. (New) A method for generating a secondary library of protein variants of a target protein comprising:
a) inputting the three dimensional coordinates of said target protein into a computer;
b) utilizing a forcefield calculation to generate a primary library comprising a plurality of primary variant amino acid residues at primary variant positions; and
c) computationally processing a plurality of said primary variant amino acid residues from step b) to generate a secondary library of secondary variant proteins, wherein at least one of said secondary variant proteins is different from the primary variant proteins.